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## RAW SEQUENCE LISTING

DATE: 01/29/2002

PATENT APPLICATION: US/09/929,313

TIME: 10:34:57

Input Set : N:\Crf3\RULE60\09929313.raw

Output Set: N:\CRF3\01292002\I929313.raw

1 <110> APPLICANT: Kao, Hung-Teh  
 2 Hartig, Paul R.  
 3 Brancheck, Theresa  
 4 <120> TITLE OF INVENTION: DNA Encoding A Human Serotonin (5-HT<sub>2</sub>) Receptor and  
 5 Uses Thereof  
 6 <130> FILE REFERENCE: 35997a3zy/JPW  
 8 <140> CURRENT APPLICATION NUMBER: 09/929,313  
 9 <141> CURRENT FILING DATE: 2001-08-14  
 11 <150> PRIOR APPLICATION NUMBER: US/09/145,864  
 12 <151> PRIOR FILING DATE: 1998-09-02  
 14 <160> NUMBER OF SEQ ID NOS: 4  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 1483  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Homo sapiens  
 21 <220> FEATURE:  
 22 <221> NAME/KEY: CDS  
 23 <222> LOCATION: (1)..(1440)  
 24 <400> SEQUENCE: 1

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26	Met Asp Ile Leu Cys Glu Glu Asn Thr Ser Leu Ser Ser Thr Thr Asn	
27	1 5 10 15	
28	tcc cta atg caa tta aat gat gac acc agg ctc tac agt aat gac ttt	96
29	Ser Leu Met Gln Leu Asn Asp Asp Thr Arg Leu Tyr Ser Asn Asp Phe	
30	20 25 30	
31	aac tcc gga gaa gct aac act tct gat gca ttt aac tgg aca gtc gac	144
32	Asn Ser Gly Glu Ala Asn Thr Ser Asp Ala Phe Asn Trp Thr Val Asp	
33	35 40 45	
34	tct gaa aat cga acc aac ctt tcc tgt gaa ggg tgc ctc tca ccg tcg	192
35	Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser	
36	50 55 60	
37	tgt ctc tcc tta ctt cat ctc cag gaa aaa aac tgg tct gct tta ctg	240
38	Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu	
39	65 70 75 80	
40	aca gcc gta gtg att att cta act att gct gga aac ata ctc gtc atc	288
41	Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile	
42	85 90 95	
43	atg gca gtg tcc cta gag aaa aag ctg cag aat gcc acc aac tat ttc	336
44	Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe	
45	100 105 110	
46	ctg atg tca ctt gcc ata gct gat atg ctg ctg ggt ttc ctt gtc atg	384
47	Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met	

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48		115		120		125		
49	ccc	gtg	tcc	atg	tta	acc	atc	ctg
50	Pro	Val	Ser	Met	Leu	Thr	Ile	Leu
51		130		135		140		
52	agc	aag	ctt	tgt	gca	gtc	tgg	att
53	Ser	Lys	Leu	Cys	Ala	Val	Trp	Ile
54		145		150		155		160
55	gcc	tcc	atc	atg	cac	ctc	tgc	gcc
56	Ala	Ser	Ile	Met	His	Leu	Cys	Ala
57				165		170		175
58	atc	cag	aat	ccc	atc	cac	cac	agc
59	Ile	Gln	Asn	Pro	Ile	His	His	Ser
60				180		185		190
61	ttt	ctg	aaa	atc	att	gct	gtt	tgg
62	Phe	Leu	Lys	Ile	Ile	Ala	Val	Trp
63			195			200		205
64	cca	ata	cca	gtc	ttt	ggg	cta	cag
65	Pro	Ile	Pro	Val	Phe	Gly	Leu	Gln
66		210				215		220
67	ggg	agt	tgc	tta	ctt	gcc	gat	gat
68	Gly	Ser	Cys	Leu	Leu	Ala	Asp	Asp
69		225			230		235	
70	gtg	tca	ttt	ttc	att	ccc	tta	acc
71	Val	Ser	Phe	Phe	Ile	Pro	Leu	Thr
72				245		250		255
73	act	atc	aag	tca	ctc	cag	aaa	gaa
74	Thr	Ile	Lys	Ser	Leu	Gln	Lys	Glu
75			260			265		270
76	ggc	aca	cgg	gcc	aaa	tta	gct	tct
77	Gly	Thr	Arg	Ala	Lys	Leu	Ala	Ser
78		275				280		285
79	ttg	tct	tca	gaa	aag	ctc	ttc	cag
80	Leu	Ser	Ser	Glu	Lys	Leu	Phe	Gln
81		290				295		300
82	tcc	tac	aca	ggc	agg	agg	act	atg
83	Ser	Tyr	Thr	Gly	Arg	Arg	Thr	Met
84		305			310		315	
85	gca	tgc	aag	gtg	ctg	ggc	atc	gtc
86	Ala	Cys	Lys	Val	Leu	Gly	Ile	Val
87			325			330		335
88	tgc	cct	ttc	ttc	atc	aca	aac	atc
89	Cys	Pro	Phe	Phe	Ile	Thr	Asn	Ile
90			340			345		350
91	tgc	aat	gag	gat	gtc	att	ggg	gcc
92	Cys	Asn	Glu	Asp	Val	Ile	Gly	Ala
93		355				360		365
94	ggt	tat	ctc	tct	tca	gca	gtc	aac
95	Gly	Tyr	Leu	Ser	Ser	Ala	Val	Asn
96		370				375		380

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97      aag acc tat agg tca gcc ttt tca cgg tat att cag tgt cag tac aag      1200
98      Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys
99      385                      390                      395                      400
100     gaa aac aaa aaa cca ttg cag tta att tta gtg aac aca ata cgg gct      1248
101     Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala
102                      405                      410                      415
103     ttg gcc tac aag tct agc caa ctt caa atg gga caa aaa aag aat tca      1296
104     Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser
105                      420                      425                      430
106     aag caa gat gcc aag aca aca gat aat gac tgc tca atg gtt gct cta      1344
107     Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu
108                      435                      440                      445
109     gga aag cag cat tct gaa gag gct tct aaa gac aat agc gac gga gtg      1392
110     Gly Lys Gln His Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val
111                      450                      455                      460
112     aat gaa aag gtg agc tgt gtg tga tag gct agt tgc cgt ggc aac tgt      1440
113     Asn Glu Lys Val Ser Cys Val                      Ala Ser Cys Arg Gly Asn Cys
W--> 114 465                      470                      475                      480
115     ggaaggcaca ctgagcaagt tttcacctat ctggtttttt ttg      1483
117 <210> SEQ ID NO: 2
118 <211> LENGTH: 471
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
121 <400> SEQUENCE: 2
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124     Ser Leu Met Gln Leu Asn Asp Asp Thr Arg Leu Tyr Ser Asn Asp Phe
125     20                      25                      30
126     Asn Ser Gly Glu Ala Asn Thr Ser Asp Ala Phe Asn Trp Thr Val Asp
127     35                      40                      45
128     Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser
129     50                      55                      60
130     Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
131     65                      70                      75                      80
132     Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile
133     85                      90                      95
134     Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe
135     100                     105                     110
136     Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met
137     115                     120                     125
138     Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro
139     130                     135                     140
140     Ser Lys Leu Cys Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr
141     145                     150                     155                     160
142     Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala
143     165                     170                     175
144     Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala
145     180                     185                     190
146     Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met

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147          195          200          205
148    Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu
149          210          215          220
150    Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe
151    225          230          235          240
152    Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu
153          245          250          255
154    Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu
155          260          265          270
156    Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser
157          275          280          285
158    Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly
159          290          295          300
160    Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys
161    305          310          315          320
162    Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp
163          325          330          335
164    Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser
165          340          345          350
166    Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile
167          355          360          365
168    Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn
169          370          375          380
170    Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys
171    385          390          395          400
172    Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala
173          405          410          415
174    Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser
175          420          425          430
176    Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu
177          435          440          445
178    Gly Lys Gln His Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val
179          450          455          460
180    Asn Glu Lys Val Ser Cys Val
181    465          470
183 <210> SEQ ID NO: 3
184 <211> LENGTH: 7
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapiens
187 <400> SEQUENCE: 3
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191 <210> SEQ ID NO: 4
192 <211> LENGTH: 471
193 <212> TYPE: PRT
194 <213> ORGANISM: Rattus norvegicus
195 <400> SEQUENCE: 4
196    Met Glu Ile Leu Cys Glu Asp Met Ile Ser Leu Ser Ser Ile Pro Met
197          1          5          10          15

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198 Ser Leu Met Asp Leu Gly Asp Gly Pro Ala Leu Val His Asn Asp Phe
199           20           25           30
200 Asn Ser Arg Asp Ala Asn Thr Ser Glu Ala Ser Asn Trp Thr Ile Asp
201           35           40           45
202 Ala Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Tyr Leu Pro Pro Thr
203           50           55           60
204 Cys Leu Ser Ile Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
205           65           70           75           80
206 Thr Thr Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile
207           85           90           95
208 Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe
209           100          105          110
210 Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met
211           115          120          125
212 Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro
213           130          135          140
214 Ser Lys Leu Cys Ala Ile Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr
215           145          150          155          160
216 Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala
217           165          170          175
218 Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala
219           180          185          190
220 Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met
221           195          200          205
222 Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu
223           210          215          220
224 Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe
225           225          230          235          240
226 Val Ala Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu
227           245          250          255
228 Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu
229           260          265          270
230 Ser Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser
231           275          280          285
232 Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly
233           290          295          300
234 Ser Tyr Ala Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys
235           305          310          315          320
236 Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp
237           325          330          335
238 Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser
239           340          345          350
240 Cys Asn Glu Asn Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile
241           355          360          365
242 Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn
243           370          375          380
244 Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys
245           385          390          395          400
246 Glu Asn Arg Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/929,313

DATE: 01/29/2002

TIME: 10:34:58

Input Set : N:\Crf3\RULE60\09929313.raw

Output Set: N:\CRF3\01292002\I929313.raw

L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1